IN THE SPECIFICATION:

Page 1, following the title, please insert the following:

-- This application is a 371 of PCT/US2003/001724 filed December 24, 2003, which is hereby incorporated by reference. --

Page 66, line 31, please insert:

-- This application claims priority to Australian application No. 2002953561 filed December 24, 2002, the entirety of which is hereby incorporated by reference. --

Page 6, lines 26-27, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Page 21, lines 1-6, should read:

(II) $R^1\text{-}Zaa_1\text{-}Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2\text{-}Haa_2\text{-}Xaa_3\text{-}Zaa_2\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R^{1'}$ (L)

[SEQ ID NO: 4, 5]

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_3, Xaa_5, Saa, Naa and L are as defined above for formula (I), m is 0 or 1, R^1 and $R^{1'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;

Page 21, lines 9-14, should read:

(III) $R^2\text{-}Zaa_1\text{-}Xaa_6\text{-}Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2\text{-}Haa_2\text{-}Zaa_2\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R^{2'}$ (L)

[SEQ ID NO: 6, 7]

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_4, Xaa_5, Saa, Naa and L are as defined above for formula (I), Xaa_6 is an amino acid residue as defined for Xaa_1 above; m is 0 or 1, R^2

and $R^{2'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;

Page 21, lines 26-21, should read:

(IV) R^3-(Haa_1-Saa-Xaa_1)$_p$-Zaa_1-Haa_2-Xaa_3-Xaa_4-Haa_3-Saa-Naa-Zaa_2-Haa_4-$R^{3'}$

[SEQ ID NO: 8, 9]

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_3, Xaa_4, Saa, Naa and L are as defined above for formula (I), p is 0 or 1, R^3 and $R^{3'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;

Page 21, lines 24-28, should read:

(V) R^4-(Haa_1-Saa-Xaa_1-Xaa_2)$_n$-Haa_2-Zaa_1-Xaa_4-Haa_3-Saa-Naa-Xaa_5-Haa_4-Zaa_2-$R^{4'}$

[SEQ ID NO: 10, 11]

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_4, Xaa_5, Saa, Naa and L are as defined above in formula (I), n is 0 or 1, R^4 and $R^{4'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L; and

Pages 21, line 30 to Page 22, line 6, should read:

(VI) R^5-(Haa_1-Saa-Xaa_1-Xaa_2)$_n$-Haa_2-Xaa_3-Zaa_1-Haa_3-Saa-Naa-Xaa_5-Haa_4-Xaa_6-Zaa_2-$R^{5'}$

[SEQ ID NO: 12, 13]

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_3, Xaa_5, Saa, Naa and L are as defined above for formula (I), Xaa_6 is an amino acid residue as defined for Xaa_1 above; n is 0 or 1, R^5 and $R^{5'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L; or a pharmaceutically acceptable salt or prodrug thereof.

Pages 22, lines 9-12, should read:

(VII) R^3-Zaa_1-Haa_2-Xaa_3-Xaa_4-Haa_3-Saa-Naa-Zaa_2-Haa_4-$R^{3'}$ **[SEQ ID NO: 14]**

wherein Zaa_1, Haa_2, Xaa_3, Xaa_4, Haa_3, Saa, Naa, Zaa_2, Haa_4, R^3, $R^{3'}$ and L are defined above in formula (IV).

Pages 22, lines 16-23, should read:

(VIII) Ac-Zaa_1-IAQELR-Zaa_2-IGDEF-NH_2 **[SEQ ID NO: 15]**

where Zaa_1 and Zaa_2 are selected from L-aspartic acid, L-glutamic acid; and
L is selected from $-NH(CH_2)_4NH-$, $-NH(CH_2)_5NH-$, $-NH(CH_2)_6NH-$, $-NH(CH_2)_7NH-$, $-NH(CH_2)_2O(CH_2)_2NH-$, $-NH(CH_2)N^+H_2(CH_2)_2NH-$, $-NH(CH_2)S(CH_2)_2NH-$, $-NHCH_2C(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)CH_2NH-$, $-NH(CH_2)_2SS(CH_2)_2NH-$, $-NH(CH_2)_2O(CH_2)_3NH-$, $-NH(CH_2)_2N^+H_2(CH_2)_3NH-$, $-NH(CH_2)_2S(CH_2)_3NH-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2NH-$ and $-NH(CH_2)_2NHC(=O)(CH_2)_2NH-$; or

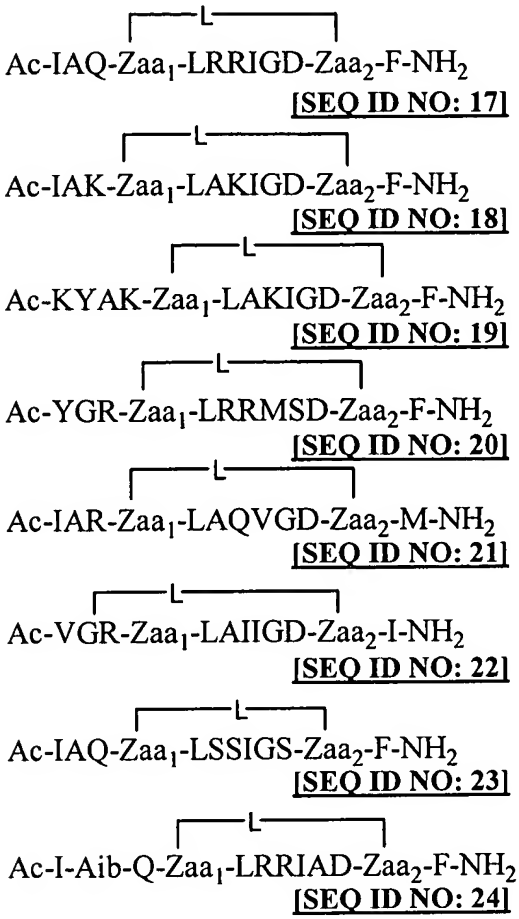
Pages 23, lines 21-24, should read:

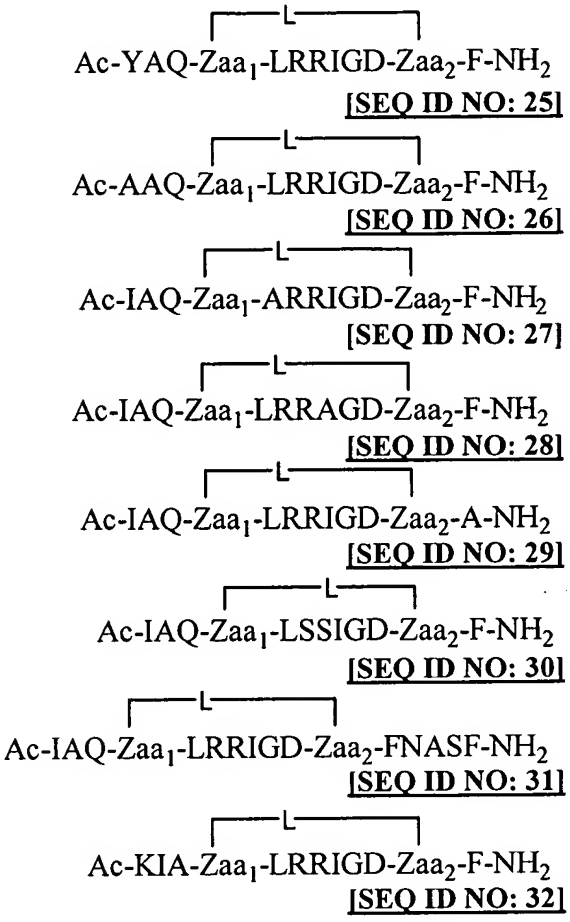
(IX) Ac-IAQ-Zaa-LRRIGD-Zaa-F-NH_2 **[SEQ ID NO: 16]**

where Zaa_1 and Zaa_2 are selected from L-aspartic acid, L-glutamic acid; and

Pages 25, lines 10-13, should read:

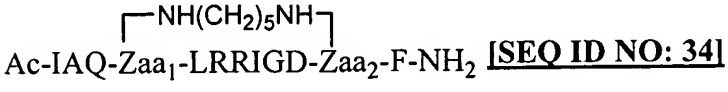
Examples of especially preferred compounds of the invention include:

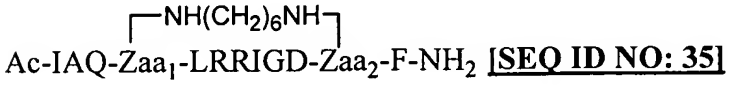


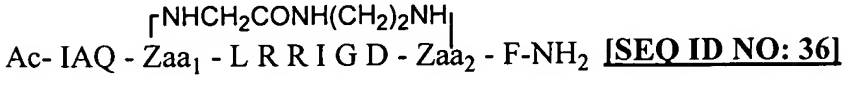


Pages 26, lines 4-8, should read:

Especially preferred compounds of the invention include:







Pages 29, lines 3-7, should read:

In another aspect of the invention there is provided a screening assay for identifying a candidate compound capable of inducing apoptosis or cell death in cells. The assay is based on the ability of candidate compounds to disrupt, or compete with, the binding of a Bim BH3 peptide comprising the sequence IAQELRRIGDEFN **[SEQ ID NO: 37]** to a Bcl-2 family protein. The BH3 peptide is preferably labelled. Preferably the Bim BH3 peptide has the sequence:

Pages 29, line 9, should read:

DLRPEIRIAQELRRIGDEFNETYTRR **[SEQ ID NO: 38]**

Pages 30, lines 1-4, should read:

IAQELRRIGDEFN **[SEQ ID NO: 39]**

under conditions sufficient to allow the candidate compound and the peptide to bind to the Bcl-2 family protein; and

Pages 31, lines 6-11, should read:

In another aspect of the invention there is provided a method of regulating the death of a cell, comprising contacting the cell with an effective amount of a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 32, line 1, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 33, line 1, should read:

I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 33, line 26, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 34, line 16, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 35, line 6, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 39, line 23, should read:

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

[SEQ ID NO: 1-3]

Pages 46, lines 17-23, should read:

Screening of the conformationally constrained peptides was performed using the Hexa-His detection system. Non biotinylated peptides dissolved in DMSO were titrated into the assay which consisted of 6-His tagged Bcl w delta C10 protein (24nM Final concentration) and Biotinylated Bim BH3-26 peptide, Biotin-DLRPEIRIAQELRRIGDEFNETYTRR **[SEQ ID NO: 40]** (1.5nM Final concentration). To this reaction mix 6His tagged (Nickel Chelate) acceptor beads and Streptavidin coated donor beads, both at 10ug/ml Final concentration, were added.

Pages 47, lines 16-23, should read:

Screening of the conformationally constrained peptides was performed using the AlphaScreen GST (glutathione S-transferase) detection kit detection system. Non biotinylated peptides dissolved in DMSO were titrated into the assay which consisted of GST tagged Bcl w delta C29 protein (0.1 nM Final concentration) and Biotinylated Bim BH3-26 peptide, Biotin-DLRPEIRIAQELRRIGDEFNETYTRR **[SEQ ID NO: 40]** (3.0 nM Final concentration). To this reaction mix anti-GST coated acceptor beads and Streptavidin coated donor beads, both at 10ug/ml Final concentration, were added and the assay mixture incubated for 4 hours at room temperature before reading.

Pages 49, lines 17-24, should read:

(a) Ac-IAQELRRIGDEF-NH_2 **[SEQ ID NO: 41]**

(b) Ac-QIAQELRRIGDEF-NH_2 **[SEQ ID NO: 42]**

(c) Ac-Z(L)IAQELRZ(L)IGDEF-NH_2 **[SEQ ID NO: 43]**

(d) Ac-IAQZ(L)LRRIGDZ(L)F-NH_2 **[SEQ ID NO: 44]**

(e) Ac-IWIAQELRRIGDEF-NH_2 **[SEQ ID NO: 45]**

(f) Ac-IZ(L)IAQELRZ(L)IGDEFNA-NH_2 **[SEQ ID NO: 46]**

(g) Ac-IWIAQZ(L)LRRIGDZ(L)FNA-NH_2 **[SEQ ID NO: 47]**

(h) Ac-IWIAQELRZ(L)IGDEFNZ(L)-NH_2 **[SEQ ID NO: 48]**

Pages 50, lines 22-23, should read:

1. The unconstrained 12-mer, (a) Ac-IAQELRRIGDEF-NH_2, **[SEQ ID NO: 41]** was relatively helically unstable.

Pages 51, lines 15-27, should read:

Example 2

The cyclic peptide Acetyl-IAQ(E1)LRRIGD(E2)F-amide **[SEQ ID NO: 41]** was synthesised using Fmoc chemistry with HTBU activation on an Applied Biosystems Pioneer peptide synthesizer. The resin used during solid phase peptide synthesis was Pal-Peg-PS resin. The base peptide was prepared using orthogonal protection on the glutamic acid residues,(E1=ODMAB, O-4-{N-[1-(4,4-dimethyl-2,6-dioxocyclohexylidene)-3-methylbutyl]amino}benzyl) and (E2=O-2-PhiPR). After synthesis E2 was deprotected selectively while the peptide was still on the resin, and a 1,5-diaminopentane (mono-Fmoc protected) linker was added to the free side chain carboxyl group. Next, the Fmoc was removed, E1 was selectively deprotected and coupled to the diaminopentane linker. The remaining protecting groups and the resin were cleaved using TFA, water, and thiol based scavengers. The peptide was then purified using RP-HPLC on a C18 YMC column. MALDI-TOF DE mass spectral analysis gave M+1: 1555.

Pages 51, lines 29-31 to Page 52, lines 1-2, should read:

Example 3

The peptide Ac-IAQ-E-LRRIGD-E-F-NH_2 **[SEQ ID NO: 41]** having a 1,6-diaminohexane linker linking the two glutamic acid residues was synthesized and purified as described in Example 2 above but using a 1,6-diaminohexane linker. MALDI-TOF DE mass spectral analysis gave M+1: 1571.

Page 52, lines 4-7, should read:

Example 4

The peptide Ac-E-IAQELR-E-IGDEF-NH_2 **[SEQ ID NO: 49]** having a 1,5-diaminopentane linker linking the two glutamic acid residues was synthesized and purified as described in Example 2 above. MALDI-TOF DE mass spectral analysis gave M+1: 1657.

Page 52, lines 9-22, should read:

Example 5

The preparation of linker precursor $NH_2CH_2CC(=O)NHCH_2CH_2NH$-Fmoc was synthesized from commercially available compounds Fmoc-$NH(CH_2)_2NH_2$.HCl (1.9g 6 mmol) and t-Boc-Gly-Osu (1.6g, 6mmol), were dissolved in DMF (15mL), then treated with N-ethyl-N,N-diisopropylamine (2.1mL, 12mmol) and stirred for 2 hours. Water (40mL) was added to precipitate the product, t-Boc-$NH_2CH_2C(=O)NHCH_2CH_2NH$-Fmoc, a colourless powder after filtering and air-drying. This was then dissolved in 4M HCl/Ether (15mL) and stood for 2 hours. The supernatant was decanted and the remaining while granules washed with ether, filtered and dried, giving the product HCl.$NH_2CH_2C(=O)NHCH_2CH_2NH$-Fmoc in 33% overall yield for the two steps. MS (m/z=340). 1H NMR (300 MHz, DMSO) δ: 8.51 (broad triplet, 1H, NH); 8.14 (broad singlet, 3H, NH_3); 7.3-7.9 (multiplet, 8H + 1H, ArH (Fmoc) + NH); 4.15-4.35 (multiplet, 3H, CH_2CH (Fmoc)); 3.49, (singlet, 2H, CH_2 (gly)); 3.15 (triplet, 2H, CH_2); 3.05 (triplet, 2H, CH_2). Chemical shift (δ) are measured in parts per million (ppm).

Page 52, lines 24-29, should read:

Example 6

The peptide Ac-IAQ-E-LRRIGD-E-F-NH_2 **[SEQ ID NO: 41]** having a -$NHCH_2C(=O)NHCH_2CH_2NH$- linker linking the two glutamic acid residues was synthesized analogously to Example 2 but using the mono-Fmoc protected linker described in Example 6, except that E1 was selectively deprotected first and reacted with the mono-Fmoc protected linker. The Fmoc was then removed and E2 was deprotected and coupled to the linker.

Page 53, lines 18-24, should read:

Example 8

The linear 16-mer peptide based on the Bim BH3-only protein, Ac-IWIAQELRRIGDEFNA-NH_2 [SEQ ID NO: 50] was prepared using a Pioneer Peptide Synthesizer and purified by HPLC. The constrained peptides were synthesized as described in Examples 2 to 6. The first constrained peptide (E) has a pentane linker tethering the two glutamate residues. The second constrained peptide (F) has a $-NHCH_2C(=O)(CH_2)_2NH_2-$ linker tethering the two glutamic acid residues.

Page 55, Table starting on line 1, should read:

Peptide	Sequence	SEQ ID	Mass Spectrometry MW	IC_{50} nM Bcl-w ΔC29
linear 16-mer	Ac-IWIAQELRRIGDEFNA-NH_2	[SEQ ID NO: 50]	1972	2.5
G (constrained)	Ac-QAIAQZLRRIGDZFNA-NH_2	[SEQ ID NO: 51]	1940	2.4
H (linear)	Ac-IWIAQQLRRIGDQFNA-NH_2	[SEQ ID NO: 52]	1969	3.3
I (linear)	Ac-IWAAQELRRIGDEFNA-NH_2	[SEQ ID NO: 53]	1930	360
J (linear)	Ac-IWIAQEARRIGDEFNA-NH_2	[SEQ ID NO: 54]	1930	3700
K (linear)	Ac-IWIAQELRRAGDEFNA-NH_2	[SEQ ID NO: 55]	1930	7.3
L (linear)	Ac-IWIAQELRRIGDEANA-NH_2	[SEQ ID NO: 56]	1896	3500
M (linear)	Ac-IWAAQEARRAGDEANA-NH_2	[SEQ ID NO: 57]	1836	64,000
N (linear)	Ac-IFIAQELRRIGDEFNA-NH_2	[SEQ ID NO: 58]	1933	11
O (linear)	Ac-AWIAQELRRIGDEFNA-NH_2	[SEQ ID NO: 59]	1930	22
P (linear)	Ac-IAIAQELRRIGDEFNA-NH_2	[SEQ ID NO: 60]	1857	42
Q (linear)	Ac-IRIAQELRRIGDEFNA-NH_2	[SEQ ID NO: 61]	1942	17
R (linear)	Ac-IWIAQELRRIGDEFAN-NH_2	[SEQ ID NO: 62]	1972	12
S (linear)	Ac-IWIAQELRRIGDEFAA-NH_2	[SEQ ID NO: 63]	1929	3.3
T (linear)	Ac-IWIAQELCitCitIGDEFNA-NH_2	[SEQ ID NO: 64]	1975	20
U (linear)	Ac-IWIAQELRRIGDEFNN-NH_2	[SEQ ID NO: 65]	2015	5.8

Page 56, lines 17-21, should read:

Example 10

Two further peptides related to Puma and Bmf BH3-only proteins were synthesized on a Pioneer peptide synthesizer and their binding affinity for Bcl-2 ΔC26 assessed.

Peptide	Sequence	SEQ ID	Mass Spectrometry MW	IC_{50} nM Bcl-w ΔC29
Puma	Ac-REIGAQLRRMADDLNA-NH_2	[SEQ ID NO: 66]	1870	52
Bmf	Ac-VQIARKLQAIADQFHR-NH_2	[SEQ ID NO: 67]	1935	0.25

Page 56, lines 22-25 to Page 57, lines1-5, should read:

Example 11

Bcl-w has been used in Examples 8 to 10 because it is a robust protein to use. However as shown below, when tested for affinity to Bcl-2 ΔC22, Bcl-w ΔC10 and Bcl-w ΔC29 using the Biacore assay and Bcl-w ΔC29 using the Alpha screen assay with GST detection, the Bim-26mer shows similar potency with respect to Bcl-w and Bcl-2. In line with the results shown in example 7, constrained peptides will also potently inhibit the binding of Bim26mer to Bcl-2 and more so than their linear counterparts.

Peptide	Sequence	IC_{50} nM Bcl-w ΔC29 Biacore	IC_{50} nM Bcl-w ΔC22 Biacore	IC_{50} nM Bcl-w ΔC10 Biacore	IC_{50} nM Bcl-w ΔC29 Alpha Screen
hsBimL/Bod (81-106)	DMRPEIWIAQELRR IGDEFNAYYARR [SEQ ID NO: 68]	4.3	2.6	6	0.1

Page 57, lines 6-12, should read:

Example 12

A retro inverso peptide having the sequence

Ac-a-n-f-e-d-g-i-r-r-l-e-q-a-i-w-i-NH_2 **[SEQ ID NO: 69]**

(Small letters refer to D-amino acids), was synthesised on an Applied Biosystems 433 Peptide Synthesiser using standard F-moc chemistry, Fields *et al.* (1991). Amino acid coupling cycles were based on manufacturers standard protocols. The peptide was purified by HPLC and molecular weight by mass spectrometry was 1971.

Page 66, at the end of the specification, please insert the printed Sequence Listing submitted concurrently herewith.